

Mon Sep 22 11:34:32 2003

us-10-026-106e-7.rmpb

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 20:57:21; Search time 282.728 seconds  
(without alignments)

13912.354 Million cell updates/sec

Title: US-10-026-106e-7

Perfected score: 1599

Sequence: 1 AAGGCGATGCGCGGCGCGA.....ACATCCGCGATGCGATG 1599

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
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16: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	1599	100.0	12 US-10-026-106e-7	Sequence 7, Appl1
2	1549.4	96.9	1563 11 US-09-995-898A-18	Sequence 16, Appl1
3	1549.4	96.9	1563 14 US-10-127-816-26	Sequence 26, Appl1
4	1354.2	84.7	1476 11 US-09-995-898A-1	Sequence 1, Appl1
5	1354.2	84.7	1476 14 US-10-137-816-23	Sequence 23, Appl1
6	1303	81.5	1472 12 US-10-026-106e-7	Sequence 9, Appl1
7	1086.8	68.0	1560 11 US-09-995-898A-28	Sequence 28, Appl1
8	915.2	57.3	1473 11 US-09-995-898A-3	Sequence 3, Appl1
9	609.4	38.1	1472 11 US-09-995-898A-32	Sequence 32, Appl1
10	609.4	38.0	1422 11 US-09-995-898A-22	Sequence 22, Appl1
11	498	31.1	674 11 US-09-995-898A-20	Sequence 20, Appl1
12	498	31.1	674 14 US-10-127-816-28	Sequence 28, Appl1
13	498	31.1	704 10 US-09-995-898A-29	Sequence 1, Appl1
14	351.2	22.0	633 11 US-10-106-698-3664	Sequence 29, Appl1
15	128	8.0	634 14 US-10-106-698-3664	Sequence 3664, Ap
16	81.4	5.1	266 13 US-10-027-632-287740	Sequence 287740,

C 17	44.4	2.8	3112	14 US-10-097-340-311	Sequence 311, App
C 18	44.4	2.8	3147	11 US-09-776-191-1	Sequence 1, Appl1
C 19	44.4	2.8	3147	11 US-09-776-191-49	Sequence 49, Appl1
C 20	44.4	2.8	3147	12 US-10-190-030B-1	Sequence 1, Appl1
C 21	44.4	2.8	3147	12 US-10-190-030B-3	Sequence 3, Appl1
C 22	44.4	2.8	3147	12 US-10-267-219-1	Sequence 1, Appl1
C 23	44.4	2.8	3147	12 US-10-267-219-3	Sequence 3, Appl1
C 24	44.4	2.8	3147	12 US-10-302-840A-1	Sequence 1, Appl1
C 25	44.4	2.8	3147	12 US-10-302-840A-3	Sequence 3, Appl1
C 26	44.4	2.8	3147	12 US-10-112-221A-1	Sequence 1, Appl1
C 27	44.4	2.8	3147	12 US-10-112-221A-3	Sequence 3, Appl1
C 28	44.4	2.8	3147	14 US-10-099-700A-3	Sequence 1, Appl1
C 29	44.4	2.8	3147	14 US-10-099-700A-3	Sequence 3, Appl1
C 30	42.2	2.6	3780	9 US-09-803-126-5	Sequence 7, Appl1
C 31	42.2	2.6	4174	9 US-09-803-126-5	Sequence 7, Appl1
C 32	40.8	2.5	5128	13 US-10-284-499-2	Sequence 2, Appl1
C 33	40.8	2.5	1223197	13 US-10-027-632-179264	Sequence 179264,
C 34	39.4	2.5	24757	10 US-09-764-868-1347	Sequence 1347, Ap
C 35	39.2	2.5	186510	12 US-10-043-715-1	Sequence 1, Appl1
C 36	38.6	2.4	597	13 US-10-027-632-105845	Sequence 105845,
C 37	38.2	2.4	597	13 US-10-027-632-105845	Sequence 105844,
C 38	38.2	2.4	598	13 US-10-027-632-209324	Sequence 209324,
C 39	38.2	2.4	660	13 US-10-027-632-18850	Sequence 18850, A
C 40	38.2	2.4	660	13 US-10-027-632-18850	Sequence 18851, A
C 41	38.2	2.4	1218	13 US-10-027-632-209323	Sequence 209323,
C 42	38	2.4	248	10 US-09-880-107-1308	Sequence 1308, Ap
C 43	38	2.4	248	10 US-09-880-107-1308	Sequence 1984, Ap
C 44	37.6	2.4	9077	9 US-09-734-300-1	Sequence 1, Appl1
C 45	37.6	2.4	9077	9 US-09-734-300-3	Sequence 3, Appl1

# ALIGNMENTS

US-10-026-106e-7	RESULT 1
/ Sequence 7, Application US/10026106E	
/ Publication No. US20030158100A1	
/ GENERAL INFORMATION:	
/ APPLICANT: Renault, Jean-Christophe	
/ APPLICANT: Fickenscher, Helmut	
/ APPLICANT: Dumoutier, Laure	
/ TITLE OF INVENTION: Isolated Cytokine Receptor LICK-2	
/ FILE REFERENCE: LUD 5752 NDH	
/ CURRENT APPLICATION NUMBER: US/10/026,106E	
/ CURRENT FILING DATE: 2001-12-21	
/ NUMBER OF SEQ ID NOS: 19	
/ SEQ ID NO 7	
/ LENGTH: 1599	
/ TYPE: DNA	
/ ORGANISM: Homo sapiens	
/ FEATURE:	
US-10-026-106e-7	
Query Match	100.0%; Score 1599, DB 12, Length 1599,
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1599; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAGGCGATGCGCGGCGCGAAGCGTGGGAGCCCTGCTCTGCTGCTGCGAGCGGCT 60
DB	1 AAGGCGATGCGCGGCGCGAAGCGTGGGAGCCCTGCTCTGCTGCTGCTGCGAGCGGCT 60
QY	61 CCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB	61 CCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY	121 GTTACTGCACTGCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB	121 GTTACTGCACTGCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY	181 ATAGAGCTCTCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240

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Db      181 ATCAGACTCTCCACCCGTAACGCTGCGCGAAGTGTGAGAGTGTGCGGAAACAAG 240
Qy      241 AGCTGTAATGTTCTATGATGTCCTGAAGAAACGAGACCTGTACAAACAGTTCCAGGGAC 300
Db      241 AGCTGTAATGTTCTATGATGTCCTGAAGAAACGAGACCTGTACAAACAGTTCCAGGGAC 300
Qy      301 GCGTGGGAGCGGTTCTCCAGCTCCAAAGTCCCCCTGGGTGGAAGTCCGAATACCTGGAAT 360
Db      301 GCGTGGGAGCGGTTCTCCAGCTCCAAAGTCCCCCTGGGTGGAAGTCCGAATACCTGGAAT 360
Qy      361 ACCTTTGTAGTGAAGCGCGGCCCCACCTGTCTGTGTCTCAACCCAGACGAGAGAGATCC 420
Db      361 ACCTTTGTAGTGAAGCGCGGCCCCACCTGTCTGTGTCTCAACCCAGACGAGAGAGATCC 420
Qy      421 TGAATGCCAATGCCAGTACAGATGCCCCCTGTGACATGCCCCCACTGGAATCTGAATATG 480
Db      421 TGAATGCCAATGCCAGTACAGATGCCCCCTGTGACATGCCCCCACTGGAATCTGAATATG 480
Qy      481 AGGTGGCATTTCTGGAAGAGAGGGGGCCGGAACCAACCTTAATTCAGTCACTCCCCATG 540
Db      481 AGGTGGCATTTCTGGAAGAGAGGGGGCCGGAACCAACCTTAATTCAGTCACTCCCCATG 540
Qy      541 GCCAGCAGTCCAGATCACTCTCCAGCAGCTGCGCAGCAACCACTGCTCAGTCCCA 600
Db      541 GCCAGCAGTCCAGATCACTCTCCAGCAGCTGCGCAGCAACCACTGCTCAGTCCCA 600
Qy      601 GAACCATCTACACCTTGAAGTGTCCCGAAATACAGCAAGTTCTTAAGCCCACTGCTTCT 660
Db      601 GAACCATCTACACCTTGAAGTGTCCCGAAATACAGCAAGTTCTTAAGCCCACTGCTTCT 660
Qy      661 TGTGTAGTCTCCAGAACGCAATGAGCTTCTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 720
Db      661 TGTGTAGTCTCCAGAACGCAATGAGCTTCTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 720
Qy      721 TGTGTATATATGCGCGCAGAGGGGTGTATCTGGAAGACCTCAATGGGGAACCCCTGATTC 780
Db      721 TGTGTATATATGCGCGCAGAGGGGTGTATCTGGAAGACCTCAATGGGGAACCCCTGATTC 780
Qy      781 AGCGGCGAAAGATGCGACGCGGCTGTGACTTTTCTGGAACAACAACCTGTGTGCAACT 840
Db      781 AGCGGCGAAAGATGCGACGCGGCTGTGACTTTTCTGGAACAACAACCTGTGTGCAACT 840
Qy      841 TTCAAGCCAGCAGACCAAGTCCGTGAATGACTTGTCTGTGTCTGTGTCTGTGTCTGTGT 900
Db      841 TTCAAGCCAGCAGACCAAGTCCGTGAATGACTTGTCTGTGTCTGTGTCTGTGTCTGTGT 900
Qy      901 CCAGAGGGGTCAAGCCGACGCTTGAAGTCAAGGCTCCAGCCCAACCAACAGATGAG 960
Db      901 CCAGAGGGGTCAAGCCGACGCTTGAAGTCAAGGCTCCAGCCCAACCAACAGATGAG 960
Qy      961 AGAAGGACCTTGCAGAGACGAAAGAGAGAGAGATGAGAGAGACAGAAATGAGCGTCA 1020
Db      961 AGAAGGACCTTGCAGAGACGAAAGAGAGAGAGATGAGAGAGACAGAAATGAGCGTCA 1020
Qy      1021 GCTTCCAGCCCTACATTTGAACAACACTTCTTCTGTGGGGCAAGAGACAAGGCTTCAGGGC 1080
Db      1021 GCTTCCAGCCCTACATTTGAACAACACTTCTTCTGTGGGGCAAGAGACAAGGCTTCAGGGC 1080
Qy      1081 ACTCGAGGCTGTGTGGGTGTGACTCAGAGAGGCGCCAGGCTCTCTGTGTCCCAAGCGAAG 1140
Db      1081 ACTCGAGGCTGTGTGGGTGTGACTCAGAGAGGCGCCAGGCTCTCTGTGTCCCAAGCGAAG 1140
Qy      1141 GCTCTCTGTGTGGGATCTTCAAGACAGAGCTGTGGGCGAGCATGTGTGATCTCTCTGTGG 1200
Db      1141 GCTCTCTGTGTGGGATCTTCAAGACAGAGCTGTGGGCGAGCATGTGTGATCTCTCTGTGG 1200
Qy      1201 ACAGGGCTGTGTCTCTGTGTGTATTTGTGTGAAGAGGGGCAAGGCGAGGGCTGTGGGG 1260
Db      1201 ACAGGGCTGTGTCTCTGTGTGTATTTGTGTGAAGAGGGGCAAGGCGAGGGCTGTGGGG 1260
Qy      1261 ATGGGACCAAGAAATCTCTCCACACAGTGAATTTCTCCAGAGACTGGGTTTCTGTGAAG 1320
Db      1261 ATGGGACCAAGAAATCTCTCCACACAGTGAATTTCTCCAGAGACTGGGTTTCTGTGAAG 1320

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Qy      1321 AGTCCCGAAGATAACTCTTCTCTGTGGGCACTGTGGGCACTTACCAACCGGAGCGA 1380
Db      1321 AGTCCCGAAGATAACTCTTCTCTGTGGGCACTGTGGGCACTTACCAACCGGAGCGA 1380
Qy      1381 ATCTGTCCCTGGGGGAGCCCGAGTTCTCTTCAAGACATGACCTTCTGTGGGAAAGCA 1440
Db      1381 ATCTGTCCCTGGGGGAGCCCGAGTTCTCTTCAAGACATGACCTTCTGTGGGAAAGCA 1440
Qy      1441 GCCCTGAGAGAGAGAGAGGCGAGGAGATCAGAAATTTGAGACACAGATGCGGGAGCT 1500
Db      1441 GCCCTGAGAGAGAGAGAGGCGAGGAGATCAGAAATTTGAGACACAGATGCGGGAGCT 1500
Qy      1501 GGGGAGCTGAGAGACACCCAGAGAGACCGAGAGACAGAGGCGGAGCAATTGGGCAATTAG 1560
Db      1501 GGGGAGCTGAGAGACACCCAGAGAGACCGAGAGACAGAGGCGGAGCAATTGGGCAATTAG 1560
Qy      1561 CCAGTGAAGTGTCTCCCGACATCCCAACCAATCTGATG 1599
Db      1561 CCAGTGAAGTGTCTCCCGACATCCCAACCAATCTGATG 1599

RESULT 2
US-09-995-898A-18
/ Sequence 18, Application US/0995898A
/ Publication No. US2003027253A1
/ GENERAL INFORMATION:
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Xu, Wenteng
/ APPLICANT: No. US2003027253A1ak, Julia E.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Grant, Francis J.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
/ FILE REFERENCE: 00-108
/ CURRENT APPLICATION NUMBER: US/09/995,898A
/ CURRENT FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: US 60/253,561
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/267,211
/ PRIOR FILING DATE: 2001-02-07
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO: 18
/ LENGTH: 1563
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1563)
US-09-995-898A-18

Query Match      96.9%; Score 1549.4; DB 11; Length 1563;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db	241	CTATGTTCTTAAGATATGTGCTGAAAGAAACAGACCTGTATACAAACAAGTTCAAGAGACCGGTG	300
Oy	306	CGGACGGTTTCTCCCACTCTCAAGTCCCTCTGGGTGGAGTCCGAATACCTGGAATTAACCTT	365
Db	301	CGGACGGTTTCTCCCACTCTCAAGTCCCTCTGGGTGGAGTCCGAATACCTGGAATTAACCTT	360
Oy	366	TTTGAATGAGACCGGACCCCACTCTCTGTGTCTACCCAGACGAGAGAAATCTTGAAT	425
Db	361	TTTGAATGAGACCGGACCCCACTCTCTGTGTCTACCCAGACGAGAGAAATCTTGAAT	420
Oy	426	GCCAATGCAAGTACAGCTGCGCCCTGTCATGCCCCCATGTGAATTAAGAGT	485
Db	421	GCCAATGCAAGTACAGCTGCGCCCTGTCATGCCCCCATGTGAATTAAGAGT	480
Oy	486	GGATTCTGGAAAGAGGGGGGCGGAAACAAAGACCTTAATTCAGATCATCTCCCATGACG	545
Db	481	GGATTCTGGAAAGAGGGGGGCGGAAACAAAGACCTTAATTCAGATCATCTCCCATGACG	540
Oy	546	CCAGTCCAGATCATCTCTCAGACAGCTGCGACGAGAACCAACATGCTCAGTGCACAGAAC	605
Db	541	CCAGTCCAGATCATCTCTCAGACAGCTGCGACGAGAACCAACATGCTCAGTGCACAGAAC	600
Oy	606	ATCTACAGTTCAAGTGTCCGAAATATAGCAAGTTCTTAAGCCCACTGCTCTTGTG	665
Db	601	ATCTACAGTTCAAGTGTCCGAAATATAGCAAGTTCTTAAGCCCACTGCTCTTGTG	660
Oy	666	GAGGTCCCAAGACGAATCTGGGCTTTCTGTGTGTGCATCGCTTGTATATCTGTGTTA	725
Db	661	GAGGTCCCAAGACGAATCTGGGCTTTCTGTGTGTGCATCGCTTGTATATCTGTGTTA	720
Oy	726	GTAAATTCGCGAGGGGTGTGATCTGGAAGACCTCATGAGGAAACCTGTGTTACGCG	785
Db	721	GTAAATTCGCGAGGGGTGTGATCTGGAAGACCTCATGAGGAAACCTGTGTTACGCG	780
Oy	786	GCAAAGATGCCAGGGGCTCTGACATTTTCTGAGACACACACCTGTGTGAACTTTTACG	845
Db	781	GCAAAGATGCCAGGGGCTCTGACATTTTCTGAGACACACACCTGTGTGAACTTTTACG	840
Oy	846	CCCAAGCAGACCAAGTCTCGTGAATGATCTTGTCTCTGTCTCCCAAAAGAACTGACAGA	905
Db	841	CCCAAGCAGACCAAGTCTCGTGAATGATCTTGTCTCTGTCTCCCAAAAGAACTGACAGA	900
Oy	906	GGGGTCAAGCGCAGACGCTGAGATCGAGGCCCCAGACCCCAACAGACAGAAATGGAAG	965
Db	901	GGGGTCAAGCGCAGACGCTGAGATCGAGGCCCCAGACCCCAACAGACAGAAATGGAAG	960
Oy	966	GACCTTGGAGAGCCAAAGAGAGAGATTAAGAGACACACAGAAATGCTGTACCTTC	1025
Db	961	GACCTTGGAGAGCCAAAGAGAGAGATTAAGAGAGACACAGAAATGCTGTACCTTC	1020
Oy	1026	CAGCCTTACATTGAACCACTTCTTTCTCTGGGGCAAGACACAGGCTTCAAGGACCTG	1085
Db	1021	CAGCCTTACATTGAACCACTTCTTTCTCTGGGGCAAGACACAGGCTTCAAGGACCTG	1080
Oy	1086	GAGGCTGGTGGGGAGACTCAGGAGAGGCCAGAGGCTCTGTGTCCAGAGAAAGGCTCC	1145
Db	1081	GAGGCTGGTGGGGAGACTCAGGAGAGGCCAGAGGCTCTGTGTCCAGAGAAAGGCTCC	1140
Oy	1146	TCTGTGTGGATTTCTTCAACAGAAAGTGGGACGACATGTGACATCTCTCTTGGACAG	1205
Db	1141	TCTGTGTGGATTTCTTCAACAGAAAGTGGGACGACATGTGACATCTCTCTTGGACAG	1200
Oy	1206	GCTGTGCTCTGTGGATTGTGCTGAGAAAGGGGACAGGCCAAGGGCCGGGTGGGATG	1265
Db	1201	GCTGTGCTCTGTGGATTGTGCTGAGAAAGGGGACAGGCCAAGGGCCGGGTGGGATG	1260
Oy	1266	CACCAAGAAATCTCTCCCAACAATCTGAATTTCCAGAGAACTGGGTTCTGTGAAGCTTC	1325
Db	1261	CACCAAGAAATCTCTCCCAACAATCTGAATTTCCAGAGAACTGGGTTCTGTGAAGCTTC	1320
Oy	1326	CCAGAAATTAACCTCTCTCTCTGTGGGACACTGGGGCACTTTACACCGGAGCCGAATCTG	1385
Db	1321	CCAGAAATTAACCTCTCTCTCTGTGGGACACTGGGGCACTTTACACCGGAGCCGAATCTG	1380

Accession	Sequence	Length
OY	1388 GTCCCTGGGGGAAACCCCAATTTCTTTCAACACTCACTCTGTGGGAAACACACCTT	1445
Db	1381 GTCCCTGGGGGAAACCCCAATTTCTTTCAACACTCACTCTGTGGGAAACACACCTT	1440
OY	1446 GAGGAGGAAGAAGGCGAGGGGATCAAGAAATTGAGCAACGATCGCGGCAACTGCGGG	1505
Db	1441 GAGGAGGAAGAAGGCGAGGGGATCAAGAAATTGAGCAACGAGATCGCGGCAACTGCGGG	1500
OY	1506 GCTGAGAGCAACCAAGAGCAACCAAGAGCAACGAGGCGCGGACATTGGGCAATTACATGGCCAG	1565
Db	1501 GCTGAGAGCAACCAAGAGCAACCAAGAGCAACGAGGCGCGGACATTGGGCAATTACATGGCCAG	1560
OY	1566 TGA 1568 	
Db	1561 TGA 1563	

RESULT 3  
 US-10-127-816-26  
 Sequence 26, Application US/10127816  
 Publication No. US20030104416A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Fox, Brian A.  
 APPLICANT: Kluecher, Kevin M.  
 APPLICANT: Taft, David W.  
 APPLICANT: Kindsvogel, Wayne R.  
 TITLE OF INVENTION: CYTOKINE PROTEIN  
 FILE REFERENCE: 01-17  
 CURRENT APPLICATION NUMBER: US/10/127, 816  
 CURRENT FILING DATE: 2002-04-19  
 PRIOR APPLICATION NUMBER: US 60/285,408  
 PRIOR FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: US 60/286,482  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: US 60/341,050  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: US 60/341,105  
 PRIOR FILING DATE: 2001-10-22  
 PRIOR APPLICATION NUMBER: US 09/895,834  
 PRIOR FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: US 60/285,424  
 PRIOR FILING DATE: 2001-04-20  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 26  
 LENGTH: 1563  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)...(1563)  
 US-10-127-816-26

	Query Match	Similarity	Score	DB	Length
Best Local	99.9%	99.9%	1549.4	14	1563
Matches	1561	Conservative	0	Mismatches	1
				Indels	1
				Gaps	1
Qy	7	ATGCGGGGGCCCGAGCGCTGGGGGCCCTCTCTGTGCTCTGACAGGCGCGCTCCAGG	66		
Dh	1	ATGCGGGGGCCCGAGCGCTGGGGGCCCTCTCTGTGCTCTGACAGGCGCGCTCCAGG	60		
Qy	67	AGGCGCGCTCTGAGCCCTCCCGAAGATGACGTCTCTCCGAACTTCAGCGGTAC	126		
Dh	61	AGGCGCGCTCTGAGCCCTCCCGAAGATGACGTCTCTCCGAACTTCAGCGGTAC	120		
Qy	127	CTGACATGAGTCCGAGAGGCTTGGAGACCCCGAATGACCTATTTTTGGTGGC-ATCAG	185		
Dh	121	CTGACATGAGTCCGAGAGGCTTGGAGACCCCGAATGACCTATTTTTGGTGGCTATCAG	180		
Qy	186	AGCTCTTCCACCCGTAGACGTGTGCGCGAAGTGAAGATGTGTCGGGAAACGAGAGCTG	245		

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Db 181 AGCTTCCACCCGTTAGACGGTGGCGGAAAGTGGAGATGTGCGGGACCAAGAGCTG 240
Qy 246 CTATGTTCTATGATGTGCTTGAAGAAACAGAGACTGTATCAACAATTCAAGGGACGGCTG 305
Db 241 CTATGTTCTATGATGTGCTTGAAGAAACAGAGACTGTATCAACAATTCAAGGGACGGCTG 300
Qy 306 CGAGCGGTTTCTCCAGCTCCAGATCCCTGGGTGAGATCCGAATPACTTGATTAACCTT 365
Db 301 CGAGCGGTTTCTCCAGCTCCAGATCCCTGGGTGAGATCCGAATPACTTGATTAACCTT 360
Qy 366 TTTGAAGTGAAGACCGGGCCCACTGTCTGTGTTCTCAACCAAGGAGAGAAATCTGAGT 425
Db 361 TTTGAAGTGAAGACCGGGCCCACTGTCTGTGTTCTCAACCAAGGAGAGAAATCTGAGT 420
Qy 426 GCCAATGCCAGTACCAAGCTGCCCCCTGATGCCCCCACTGAGATCTGAATGAGGTG 485
Db 421 GCCAATGCCAGTACCAAGCTGCCCCCTGATGCCCCCACTGAGATCTGAATGAGGTG 480
Qy 486 GCATTCTGGAAGAGAGGGGGCGGAAACAAGACCTTATTTCCAGTCACTCCCAATGGCCAG 545
Db 481 GCATTCTGGAAGAGAGGGGGCGGAAACAAGACCTTATTTCCAGTCACTCCCAATGGCCAG 540
Qy 546 CCAAGTCCAGATCACTTCCAGCCAGCTGCGAGGAAACAACAATGCTGATGCGAGAAC 605
Db 541 CCAAGTCCAGATCACTTCCAGCCAGCTGCGAGGAAACAACAATGCTGATGCGAGAAC 600
Qy 606 ATCTACACGTTCAATGTGCTCCGAAATACAGCAAGTTCTCTAAGCCCAAGCTGCTTGTG 665
Db 601 ATCTACACGTTCAATGTGCTCCGAAATACAGCAAGTTCTCTAAGCCCAAGCTGCTTGTG 660
Qy 666 GAGGTCCCAAGAACCAATGCGCTTTCTGTGTGCTGCAATGCTTCTGATTAAGCTGTTA 725
Db 661 GAGGTCCCAAGAACCAATGCGCTTTCTGTGTGCTGCAATGCTTCTGATTAAGCTGTTA 720
Qy 726 GTAAATGCGCAGGGGGTGTGATCTGGAAGAACCTCATGGGAAACCTTGATTTACGCGG 785
Db 721 GTAAATGCGCAGGGGGTGTGATCTGGAAGAACCTCATGGGAAACCTTGATTTACGCGG 780
Qy 786 GCAAAGATGCGACGGGGCTGAGATTTTCTGGAACAACAACCTGTGAGCAACTTTACG 845
Db 781 GCAAAGATGCGACGGGGCTGAGATTTTCTGGAACAACAACCTGTGAGCAACTTTACG 840
Qy 846 CCCAGAGACCAAGATCCGTGAATGACTTGTCTGTGCTCCCAAGAGAACTGACCAAG 905
Db 841 CCCAGAGACCAAGATCCGTGAATGACTTGTCTGTGCTCCCAAGAGAACTGACCAAG 900
Qy 906 GGGGTCAAGGCCGACCGCTGAGTCAAGGGCCCAAGCCCAACAAGATGGAAGAG 965
Db 901 GGGGTCAAGGCCGACCGCTGAGTCAAGGGCCCAAGCCCAACAAGATGGAAGAG 960
Qy 966 GACCTTGCAGAGAGCAAGAGAGAGAGATGAGAGAGACAAGAGATGGCGTCAAGCTTC 1025
Db 961 GACCTTGCAGAGAGCAAGAGAGAGAGATGAGAGAGACAAGAGATGGCGTCAAGCTTC 1020
Qy 1026 CAGCCCTCAATTTGAACAACCTTTCTTCTGAGGCAAGAGACAAGAGCTCCAGGCACTG 1085
Db 1021 CAGCCCTCAATTTGAACAACCTTTCTTCTGAGGCAAGAGACAAGAGCTCCAGGCACTG 1080
Qy 1086 GAGGCTGTGGGGTGAATCTCAAGAGGCCCAAGGGCTCTCTGTGTTCCCAAGGAGCTCC 1145
Db 1081 GAGGCTGTGGGGTGAATCTCAAGAGGCCCAAGGGCTCTCTGTGTTCCCAAGGAGCTCC 1140
Qy 1146 TCTGCTTGGGATTTCTTCAAGACAGAGCTGGGCAAGCACTGCTCTCTGAGGACAG 1205
Db 1141 TCTGCTTGGGATTTCTTCAAGACAGAGCTGGGCAAGCACTGCTCTCTGAGGACAG 1200
Qy 1206 GCTGGGCTCTCTGCTAATTTGGCTGAAGAGGGCCAGGCGGGCTGGGTGAGATGG 1265
Db 1201 GCTGGGCTCTCTGCTAATTTGGCTGAAGAGGGCCAGGCGGGCTGGGTGAGATGG 1260
Qy 1266 CACCAAGAAATCTCTCCACAACCTGAATTTCTCAAGAGACTGGGATTTCTTGAAGAGCTC 1325
Db 1261 CACCAAGAAATCTCTCCACAACCTGAATTTCTCAAGAGACTGGGATTTCTTGAAGAGCTC 1320

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Qy 1326 CCAGAAATTAACCTCTCTCTCTGAGGCACTTGAAGGCACTTACACCGGAGCCGAATCTG 1385
Db 1321 CCAGAAATTAACCTCTCTCTCTGAGGCACTTGAAGGCACTTACACCGGAGCCGAATCTG 1380
Qy 1386 GTCCCTGGGGAGCCCCCAAGTTTCTTCAAGACATGACCTTTGTGAGGAAAGACAGCCCT 1445
Db 1381 GTCCCTGGGGAGCCCCCAAGTTTCTTCAAGACATGACCTTTGTGAGGAAAGACAGCCCT 1440
Qy 1446 GAGAGAGAAAGAGAGGCGAGGAAATCAAAATTTGAAGACAGCAATCGGGCAGCTGGGG 1505
Db 1441 GAGAGAGAAAGAGAGGCGAGGAAATCAAAATTTGAAGACAGCAATCGGGCAGCTGGGG 1500
Qy 1506 GCTGAGAGCAACCCAGAGGACCCAGAGACAGGGCCGGAATTGGGGCATTAACAATGGCCAG 1565
Db 1501 GCTGAGAGCAACCCAGAGGACCCAGAGACAGGGCCGGAATTGGGGCATTAACAATGGCCAG 1560
Qy 1566 TGA 1568
Db 1561 TGA 1563

RESULT 4
US-09-995-898A-1
; Sequence 1, Application US/0995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: No. US20030027253A1a, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1473)
US-09-995-898A-1

Query Match 84.7%; Score 1354.2; DB 11; Length 1476;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 8; Indels 88; Gaps 2;

Qy 7 ATGCGGGGGCCCAAGGCTGGGGCCCTGCTCTGTGCTCTGAGGCGGCTCCAGG 66
Db 1 ATGCGGGGGCCCAAGGCTGGGGCCCTGCTCTGTGCTCTGAGGCGGCTCCAGG 60
Qy 67 AGGCGCGGTGCGCCCTCCCAAGATGACGCTGCTCTCCAGAACTTACAGCGTATC 126
Db 61 AGGCGCGGTGCGCCCTCCCAAGATGACGCTGCTCTCCAGAACTTACAGCGTATC 120
Qy 127 CTGACATGAGTCCCAAGGCTTGGCAACCCCAAGATGACATTTTGTGGCC-ATGAG 185
Db 121 CTGACATGAGTCCCAAGGCTTGGCAACCCCAAGATGACATTTTGTGGCC-ATGAG 180
Qy 186 AGCTCTCCACCCGTGAGACGATGGCGGCAAGTGAAGATGTGCGGGAACAAGAGCTG 245
Db 181 AGCTCTCCACCCGTGAGACGATGGCGGCAAGTGAAGATGTGCGGGAACAAGAGCTG 240
Qy 246 CTATGTTCTATGATGTGCTTGAAGAAACAGAGACTGTATCAACAATTCAAGGGACGGCTG 305

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Db 241 CTATGTTCTATGATGTCCTGAGAAACAGACCTGTACACAAAGTTCAAGGAGCGCTG 300  
 QY CGACAGGTTTCTCCAGCTTCAGAGTCCCTGGGTGAGTCCGAATTAACCTT 365  
 Db 301 CGACAGGTTTCTCCAGCTTCAGAGTCCCTGGGTGAGTCCGAATTAACCTT 360  
 QY 366 TTGGAAGTGGAGCCGAGCCCACTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 425  
 Db 361 TTGGAAGTGGAGCCGAGCCCACTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 420  
 QY 426 GCCAATGCCCATTAACAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 485  
 Db 421 GCCAATGCCCATTAACAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 480  
 QY 486 GCATTCTGGAAGAGAGGAGGAGCCGAGAAACAAAGACCTATTTCCAGTCACTCCAGAGCGAG 545  
 Db 481 GCATTCTGGAAGAGAGGAGGAGCCGAGAAACAAAGACCTATTTCCAGTCACTCCAGAGCGAG 540  
 QY 546 CCAAGTCCAGATCACTCTCCAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 605  
 Db 541 CCAAGTCCAGATCACTCTCCAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 600  
 QY 606 ATCTACACGTTCAAGTCTCCGAAATACAGCAAGTCTCTAAGCCCACTGCTTCTTGTG 665  
 Db 601 ATCTACACGTTCAAGTCTCCGAAATACAGCAAGTCTCTAAGCCCACTGCTTCTTGTG 660  
 QY 666 GAGGTCCGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 725  
 Db 661 GAGGTCCGAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 QY 726 GTAATTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 785  
 Db 721 GTAATTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 QY 786 GCAAAAGTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 845  
 Db 781 GCAAAAGTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800  
 QY 846 CCAAGTCCAGATCACTCTCCAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 905  
 Db 801 CCAAGTCCAGATCACTCTCCAGCTGCTGCTGCTCAACCCAGACGAGAGATCCTGAGT 900  
 QY 906 GGGGTGAGGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 965  
 Db 814 GGGGTGAGGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873  
 QY 966 GACCTTGCAG 1025  
 Db 874 GACCTTGCAG 933  
 QY 1026 CAGCCCTTACATTAACAGCTTCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1085  
 Db 934 CAGCCCTTACATTAACAGCTTCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993  
 QY 1086 GAG 1145  
 Db 994 GAG 1053  
 QY 1146 TGTGCTTGGAGATCTTTCAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205  
 Db 1054 TGTGCTTGGAGATCTTTCAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1113  
 QY 1206 GGTGAG 1265  
 Db 1114 GGTGAG 1173  
 QY 1266 CACCAAGAGATCTTCTCCAGCACTGAAATCTTCCAGAGAGATCTGAGAGAGAGCTT 1325  
 Db 1174 CACCAAGAGATCTTCTCCAGCACTGAAATCTTCCAGAGAGATCTGAGAGAGAGCTT 1233  
 QY 1326 CCAAGAGAGATCTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385  
 Db 1234 CCAAGAGAGATCTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1293

QY 1386 GTCCCTGGGAGAGCCCGAGTTTCTCTTACAGACAGTCACTTCTGCTGGAGAGAGAGCCCT 1445  
 Db 1294 GTCCCTGGGAGAGCCCGAGTTTCTCTTACAGACAGTCACTTCTGCTGGAGAGAGAGCCCT 1353  
 QY 1446 GAG 1505  
 Db 1354 GAG 1413  
 QY 1506 GCTGAG 1565  
 Db 1414 GCTGAG 1473  
 QY 1566 TGA 1568  
 Db 1474 TGA 1476  
 RESULT 5  
 US-10-127-816-23  
 ; Sequence 23, Application US/10127816  
 ; Publication No. US20030104416A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Fox, Brian A.  
 ; APPLICANT: Kluehner, Kevin M.  
 ; APPLICANT: Tate, David W.  
 ; APPLICANT: Kindsvogel, Wayne R.  
 ; TITLE OF INVENTION: CYTOKINE PROTEIN FAMILY  
 ; FILE REFERENCE: 01-17  
 ; CURRENT APPLICATION NUMBER: US/10/127,816  
 ; PRIOR FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: US 60/285,408  
 ; PRIOR FILING DATE: 2001-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/286,482  
 ; PRIOR FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: US 60/341,050  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/341,105  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 09/895,834  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/285,424  
 ; PRIOR FILING DATE: 2001-04-20  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO: 23  
 ; LENGTH: 1476  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1473)  
 ; US-10-127-816-23  
 Query Match 84.7%, Score 1354.2, DB 14, Length 1476,  
 Best Local Similarity 93.9%, Pred. No. 0,  
 Matches 1467, Conservative 0, Mismatches 8, Indels 88, Gaps 2,  
 QY 7 ATGGGGGGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66  
 Db 1 ATGGGGGGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60  
 QY 67 AGGCGCGGTGAGCCCTCCCGAGATGAGAGCTGCTCTCCAGAGATTCAGAGCTGTAC 126  
 Db 61 AGGCGCGGTGAGCCCTCCCGAGATGAGAGCTGCTCTCCAGAGATTCAGAGCTGTAC 120  
 QY 127 CTGACATGAGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185  
 Db 121 CTGACATGAGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 186 AGCTTCCCAACCGTGAACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245

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Db 181 AGCTCCACCCGTTAGACGGTGGCGGAAAGTGAAGTGTGGGGAACCAAGAGCTG 240.
Qy 246 CTATGTTCTATGATGTGCTGTAAGAAAACAGAACCTGTACACAACTTCAAGGACCCGTT 305
Db 241 CTATGTTCTATGATGTGCTGTAAGAAAACAGAACCTGTACACAACTTCAAGGACCCGTT 300
Qy 306 CGGACGGTTCCTCCAGCTCCAGATCCCTGGGAGTGAATCCGAATACCTGATTAACCTT 365
Db 301 CGGACGGTTCCTCCAGCTCCAGATCCCTGGGAGTGAATCCGAATACCTGATTAACCTT 360
Qy 366 TTTGAAGTGAAGCCGGGCCCCCACTGTCTGTGTGTCACTCCAGACGAGAGAGATCTTGAT 425
Db 361 TTTGAAGTGAAGCCGGGCCCCCACTGTCTGTGTGTCACTCCAGACGAGAGAGATCTTGAT 420
Qy 426 GCCAATGCGCATACAGCTGCCCCCTGTGATGCCCCCACTGTGATGAGTGAAGTGAAGT 485
Db 421 GCCAATGCGCATACAGCTGCCCCCTGTGATGCCCCCACTGTGATGAGTGAAGTGAAGT 480
Qy 486 GCAATTCGGAAGAGAGGGGGCCGGAACAAAGACCTATTTCCAGTCACTCCCAATGGCCAG 545
Db 481 GCAATTCGGAAGAGAGGGGGCCGGAACAAAGACCTATTTCCAGTCACTCCCAATGGCCAG 540
Qy 546 CCAGTCAGATCACTCTCCAGCCAGCTGCGAGCGAAACACATGTCCTAGTGCAGAAC 605
Db 541 CCAGTCAGATCACTCTCCAGCCAGCTGCGAGCGAAACACATGTCCTAGTGCAGAAC 600
Qy 606 ATCTACAGCTTCACTGTGCTCCGAAATACAGCAAGTCTCTAAGCCCACTGCTTCTTGCT 665
Db 601 ATCTACAGCTTCACTGTGCTCCGAAATACAGCAAGTCTCTAAGCCCACTGCTTCTTGCT 660
Qy 666 GAGCTCCCAAGAACGAACTGGGCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
Db 661 GAGCTCCCAAGAACGAACTGGGCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 726 GTAAATGCGCGAGGGGGTGTATGTGAAGAACCTTCATATGGGAAACCTGATTTACGCG 785
Db 721 GTAAATGCGCGAGGGGGTGTATGTGAAGAACCTTCATATGGGAAACCTGATTTACGCG 780
Qy 786 GCAAAAGTCCACGGGCGCTGTGACTTTTCTGGAACACACACCTGTGGCACTTTGAG 845
Db 781 GCAAAAGTCCACGGGCGCTT----- 800
Qy 846 CCCAGACACAGAGTCCGTGATGACTTGTCTCTGTCTCCCAAGAAAGAACTGACAGAG 905
Db 801 -----GAACTGACAGAG 813
Qy 906 GGGGTGAGGCGAGGCTCGAGTGAAGGGCCCAAGCCCAACAGACAGAAATGGAAGAG 965
Db 814 GGGGTGAGGCGAGGCTCGAGTGAAGGGCCCAAGCCCAACAGACAGAAATGGAAGAG 873
Qy 966 GACCTTGCAGAGACGAAAGAGAGAGATGAGAGAGACACAGAAATGGCGTCACTTC 1025
Db 874 GACCTTGCAGAGACGAAAGAGAGAGATGAGAGAGACACAGAAATGGCGTCACTTC 933
Qy 1026 CAGCCCTACATTGAACCACTTTCTGTGTGGGCAAGACACAGGCTCCAGGGCACTG 1085
Db 934 CAGCCCTACATTGAACCACTTTCTGTGTGGGCAAGACACAGGCTCCAGGGCACTG 993
Qy 1086 GAGGCTGTGGGGTGAATCAAGGAGGGCCCAAGGCTCTCTGTGTGTCCAGGAAAGCTTC 1145
Db 994 GAGGCTGTGGGGTGAATCAAGGAGGGCCCAAGGCTCTCTGTGTGTCCAGGAAAGCTTC 1053
Qy 1146 TCTGTGTGGGATTTCTTCAAGACAGAGTGGGCAAGCACTGTGATCTCTCTGGAACAG 1205
Db 1054 TCTGTGTGGGATTTCTTCAAGACAGAGTGGGCAAGCACTGTGATCTCTCTGGAACAG 1113
Qy 1206 GCTGGGTCTCTGTGTATTTGGCTGAAGAGGGCCAGGCTCAAGGGCCGGGTGGGATGG 1265
Db 1114 GCTGGGTCTCTGTGTATTTGGCTGAAGAGGGCCAGGCTCAAGGGCCGGGTGGGATGG 1173
Qy 1266 CACCAAGAAATCTCTCCACACACTGAATTTCTCAAGAGACTGGGTTTCTGTGAAGACTC 1325
Db 1174 CACCAAGAAATCTCTCCACACACTGAATTTCTCAAGAGACTGGGTTTCTGTGAAGACTC 1233

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Qy 1326 CCAGAAATTAACCTCTCTCTGTGGGCACTGTGGGCACTTTACACCGGAAGCCGAATCTG 1385
Db 1234 CCAGAAATTAACCTCTCTCTGTGGGCACTGTGGGCACTTTACACCGGAAGCCGAATCTG 1293
Qy 1386 GTCCCTGGGGAACCCCAAGTTTCTCTTCAAGACATGACCTTGTGTGGGAAGAGCCCT 1445
Db 1294 GTCCCTGGGGAACCCCAAGTTTCTCTTCAAGACATGACCTTGTGTGGGAAGAGCCCT 1353
Qy 1446 GAGAGGAAGAGAGGCGAGGGAATCAGAAATTGAGAGACAGATGCGGGGAGCTGGGG 1505
Db 1354 GAGAGGAAGAGAGGCGAGGGAATCAGAAATTGAGAGACAGATGCGGGGAGCTGGGG 1413
Qy 1506 GCTGAGACACCCAGAGAGCCAGAGACAGGGCCGAGCATTTGGGAGCATTAATGCGCAG 1565
Db 1414 GCTGAGAGACACCCAGAGAGCCAGAGACAGGGCCGAGCATTTGGGAGCATTAATGCGCAG 1473
Qy 1566 TGA 1568
Db 1474 TGA 1476

RESULT 6
US-10-026-106E-9
; Sequence 9, Application US/10026106E
; Publication No. US20030158100A1
; GENERAL INFORMATION:
; APPLICANT: Renault, Jean-Christophe
; APPLICANT: Fickenslecher, Helmut
; APPLICANT: Dumoutier, Laure
; TITLE OF INVENTION: Isolated Cytokine Receptor Lich-2
; FILE REFERENCE: LUD 5752 NDH
; CURRENT APPLICATION NUMBER: US/10/026, 106E
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 9
; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-026-106E-9

Query Match      81.5%; Score 1303; DB 12; Length 1472;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1468; Conservative 0; Mismatches 0; Indels 135; Gaps 3;

Qy 1 AAGGCAATGGCGGGGCGCGAGGCTGGGGGCCCCCTGTCTGTGTGCTGTGAGGCGGCT 60
Db 1 AAGGCAATGGCGGGGCGCGAGGCTGGGGGCCCCCTGTCTGTGTGCTGTGAGGCGGCT 60
Qy 61 CCAGGAGGCGCCGCTGTGGCCCTTCCAGAAATGTAAGCTGTCTCCAGAACTTCAGC 120
Db 61 CCAGGAGGCGCCGCTGTGGCCCTTCCAGAAATGTAAGCTGTCTCCAGAACTTCAGC 120
Qy 121 GTTAACTGAATAGGCTCCAGAGGCTTGGCAACCCCAAGAAATGTAACCTATTGTGGCC 180
Db 121 GTTAACTGAATAGGCTCCAGAGGCTTGGCAACCCCAAGAAATGTAACCTATTGTGGCC 180
Qy 181 -ATCAGAGCTCTCCACCCGTTGAGACGATGGCGTGAAGATGAGTGGGGAACAAAG 239
Db 181 TATCAGAGCTCTCCACCCGTTGAGACGATGGCGTGAAGATGAGTGGGGAACAAAG 240
Qy 240 GAGCTGTATGTTCTATGATGTGCTGAAAGAAACAGGACCTGTACAAAGTTCAAGGGA 299
Db 241 GAGCTGTATGTTCTATGATGTGCTGAAAGAAACAGGACCTGTACAAAGTTCAAGGGA 300
Qy 300 CGCGTGTGAGCGGTTCTCCAGCTCCAGATGCTCCCTGTGGTGAAGTCCGAATACCTGGAT 359
Db 301 CGCGTGTGAGCGGTTCTCCAGCTCCAGATGCTCCCTGTGGTGAAGTCCGAATACCTGGAT 360
Qy 360 TACCTTTTGAATGAGCGGGCCCACTGTCTGTGTGCTCAACCGAGACGAGAGATC 419

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Db 361 TACCTTTTGAAGTGAAGGCGGCGCCACCTGTCCTGTCCTACCCAGAGAGATC 420  
 Qy 420 CTGATTTGCCATATGCCATCTACAGCTGCCCCCTGATGCCCCCACTGAAATTTAA 479  
 Db 421 CTGATGTCGAATGCAAGTCAAGCTGCCCCCTGATGCCCCCACTGAAATTTAA 480  
 Qy 480 GAGTGGGATTTCTGGAAGAGGAGGCGGAAACAAGACCTATTTCAGTCACTCCCAT 539  
 Db 481 GAGTGGGATTTCTGGAAGAGGAGGCGGAAACAAGACCTATTTCAGTCACTCCCAT 540  
 Qy 540 GGGCAGGCGAGTCCAGATCACTCTCCAGCGAGTCCAGCAACAACCTGCTCACTGTC 599  
 Db 541 GGGCAGGCGAGTCCAGATCACTCTCCAGCGAGTCCAGCAACAACCTGCTCACTGTC 600  
 Qy 600 AGAACCATCTACAGCTTCACTGTCCTGGAATTAAGCAAGTCTCTAAGCCCACTGTC 659  
 Db 601 AGAACCATCTACAGCTTCACTGTCCTGGAATTAAGCAAGTCTCTAAGCCCACTGTC 660  
 Qy 660 TTGCTGAGAGTCCCAAGAGGAACTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTG 719  
 Db 661 TTGCTGAGAGTCCCAAGAGGAACTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTG 719  
 Qy 720 CTGTTAGTAAATTCGCGAGGAGGCTGATCTGGAAGACCTCATGGGAAACCCCTGCTT 779  
 Db 676 ----- 675  
 Qy 780 CAGCGGCGAAAGATGCGAGGCGCTGGAATTTCTGGAACAACAACCTGCTGGAAC 839  
 Db 676 ----- GAGCTTTCTGGAACAACAACCTGCTGGAAC 709  
 Qy 840 TTTCAAGCCCAAGACCAAGTCCGTAATGAATTTCTGCTGCTGCTGCTGCTGCTG 899  
 Db 710 TTTCAAGCCCAAGACCAAGTCCGTAATGAATTTCTGCTGCTGCTGCTGCTGCTG 769  
 Qy 900 ACCAGAGGAGTCAAGGCGAGCGCTGAGTCAAGGCGCGCAACCCCAAGCAAGAGATG 959  
 Db 770 ACCAGAGGAGTCAAGGCGAGCGCTGAGTCAAGGCGCGCAACCCCAAGCAAGAGATG 829  
 Qy 960 AAGAAAGACCTTTCAGAGAGCAAGAGAGAGAGATGAAGAGCAACAAGATGCGCTC 1019  
 Db 830 AAGAAAGACCTTTCAGAGAGCAAGAGAGAGAGATGAAGAGCAACAAGATGCGCTC 889  
 Qy 1020 AGCTTCCAGGCTCACTTGAACCACTTCTTCTGAGGAGCAAGAGCAAGGCTCAAGG 1079  
 Db 890 AGCTTCCAGGCTCACTTGAACCACTTCTTCTGAGGAGCAAGAGCAAGGCTCAAGG 949  
 Qy 1080 CACTCGAGAGC---TGTGGGTGAGTCAAGAGAGCGCCAGGCTCTCTGCTGCTCAAGC 1136  
 Db 950 CACTCGAGAGC---TGTGGGTGAGTCAAGAGAGCGCCAGGCTCTCTGCTGCTCAAGC 1009  
 Qy 1137 GAAGGCTCTCTGCTGAGATTTCAAGAGAGTGGGCGAGCACTGTAATCTCTCC 1196  
 Db 1010 GAAGGCTCTCTGCTGAGATTTCAAGAGAGTGGGCGAGCACTGTAATCTCTCC 1069  
 Qy 1197 TGGGAGAGGCTGGGCTCTGAGATTTGCTGAGAGAGGCGAGGCGAGGCGAGGCT 1256  
 Db 1070 TGGGAGAGGCTGGGCTCTGAGATTTGCTGAGAGAGGCGAGGCGAGGCGAGGCT 1129  
 Qy 1257 GGGGATGGGAGCAAGAAATCTCTCCAGCACTGTAATTTCTCAAGAGCTCGGATTTCTG 1316  
 Db 1130 GGGGATGGGAGCAAGAAATCTCTCCAGCACTGTAATTTCTCAAGAGCTCGGATTTCTG 1189  
 Qy 1317 GAAGAGCTCCAGAAAGATTAATCTCTCCCTGAGGCGAGCTGGGAGCACTTCAACCGAG 1376  
 Db 1190 GAAGAGCTCCAGAAAGATTAATCTCTCTCTGAGGCGAGCTGGGAGCACTTCAACCGAG 1249  
 Qy 1377 CCGAATCTGCTGCTGGGAGACCCCGAGTTTCTTCTCAAGCACTGATCTTCTGCTGAGAA 1436  
 Db 1250 CCGAATCTGCTGCTGGGAGACCCCGAGTTTCTTCTCAAGCACTGATCTTCTGCTGAGAA 1309  
 Qy 1437 AGCAGCCTGAG 1496  
 Db 1310 AGCAGCCTGAG 1369

Qy 1497 AGCTGGGGGCTGAG 1556  
 Db 1370 AGCTGGGGGCTGAG 1429  
 Qy 1557 ATGGCCAGGAG 1599  
 Db 1430 ATGGCCAGGAG 1472

RESULT 7  
 US-09-995-898A-28  
 ; Sequence 28, Application US/0995898A  
 ; Publication No. US20030027253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parnell, Scott R.  
 ; APPLICANT: Xu, Wenfeng  
 ; APPLICANT: No. US20030027253A1ak, Julia E.  
 ; APPLICANT: Whitmore, Theodore E.  
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
 ; FILE REFERENCE: 00-108  
 ; CURRENT FILING DATE: US/09/995, 898A  
 ; PRIOR APPLICATION NUMBER: US 60/253,561  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/267,211  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 28  
 ; LENGTH: 1560  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Degenerate Polynucleotide sequence of SEQ ID  
 ; OTHER INFORMATION: NO:19  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(1560)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-995-898A-28

Query Match 68.0%; Score 1086.8; DB 11; Length 1560;  
 Best Local Similarity 57.0%; Pred. No. 2.9e-308;  
 Matches 888; Conservative 355; Mismatches 315; Indels 1; Gaps 1;

Qy 7 ATGGCGGGGCGGAGGCGCTGAGGCGGCGGCTGAGGCGGCGGCGGCGGCGGCGGCGG 66  
 Db 1 ATGGCGGCGGCGGAGGCGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
 Qy 67 AGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126  
 Db 61 AGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 Qy 127 CTGAGATGAGCTCCAGAGGCTGAGCAACCCAGAGATGAGCTTATTTTGTGGCC-ATCAG 185  
 Db 121 YTNACGTTGTTGCGGAGTGTGTTAABARCARAYTTTAAVARTTAAABGGGNGTIN 180  
 Qy 186 AGCTCTCCACCGCTAGACGCTGAGGCGGAGAGAGAGTGTGGGAGACCAAGAGCTG 245  
 Db 181 MSNMSNCNACNM 240  
 Qy 246 CTATGTTCTATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305  
 Db 241 YTNATGMSNATGATGATGTTAABARCARAYTTTAAVARTTAAABGGGNGTIN 300  
 Qy 306 CGGAGGTTTCTCCAGAGTCCCAAGTCCCGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 365  
 Db 301 MGNACGNTMNCNM 360  
 Qy 366 TTGGAAGTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 425



486 GCATTGGAAGAGGGGGCCGGAACAGACCTATTTCAGTCACTCCCATGCGAG 545  
481 GCTTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
546 CCACTCCAGATCACTCTCCAGCAGCTCCAGGAGAGACCACTGCTCAGTCCAGAAC 605  
541 CCGTGCATATATACCTTATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
606 ATCTACAGCTTCACTGCTCCGGAATACAGCAAGTCTCTAAGCCACTGCTCTTCTG 665  
601 ATTTATACCTTAT 660  
666 GAGTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 725  
661 GAGTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
726 GTAAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 785  
721 GTATATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
786 GCAAGAGTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 845  
781 GCAAGAGTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
846 CCCAGAGAGCAGAGTCCGTAATGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 905  
801 -----NGARTNACNNGN 813  
906 GGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 965  
814 GGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873  
966 GAGTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1025  
874 GAYTTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 933  
1026 CAGGCTTCACTTGAACCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1085  
934 CAGGCTTCACTTGAACCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 993  
1086 GAGGCTTCACTTGAACCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1145  
994 GAGGCTTCACTTGAACCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1053  
1146 TCTGCTTGGGATTTCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205  
1054 TCTGCTTGGGATTTCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1113  
1206 GCTGAGTCTCTGAGTATTTGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1265  
1114 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1173  
1266 CAGGAGATCT 1325  
1174 CAGGAGATCT 1233  
1326 CAGGAGATCT 1385  
1234 CAGGAGATCT 1293  
1386 GTCCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1445  
1294 GTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1353  
1446 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505  
1354 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1413  
1506 GCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1564  
1414 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1472

RESULT 9  
US-09-995-898A-32  
Sequence 32, Application US/0995898A  
Publication No. US2003027253A1  
GENERAL INFORMATION:  
APPLICANT: Presnell, Scott R.  
APPLICANT: Xu, Wenteng  
APPLICANT: No. US2003027253A1, Julia E.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Grant, Francis J.  
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19  
FILE REFERENCE: 00-108  
CURRENT APPLICATION NUMBER: US/09/995,898A  
CURRENT FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: US 60/253,561  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 60/267,211  
PRIOR FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 1922  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: MBP-human zcytor19 fusion protein polynucleotide  
OTHER INFORMATION: sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (123)...(1922)  
US-09-995-898A-32  
Query Match 38.1%; Score 609.4; DB 11; Length 1922;  
Best Local Similarity 97.4%; Pred. No. 2.7e-168;  
Matches 630; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
46 CTGCTGACAGGCGGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 105  
1266 CCGCTGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1325  
106 TCCGAGAGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165  
1326 TCCGAGAGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385  
166 ACCTATTTTGGGCT-ATCAGAGCTCTCCACCGGTAGAGCGGTGAGGAGGAGGAGGAGGAG 224  
1386 ACCTATTTTGGGCTATCAGAGCTCTCCACCGGTAGAGCGGTGAGGAGGAGGAGGAGGAG 1445  
226 TGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 284  
1446 TGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505  
286 AACCAAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 344  
1506 AACCAAGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1565  
346 TCCGAGATCTGAGATTAAGTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404  
1566 TCCGAGATCTGAGATTAAGTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1625  
406 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 464  
1626 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1685  
466 CTGAGTCTGAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524  
1686 CTGAGTCTGAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1745  
526 CCAATCACTCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 584  
1746 CCAATCACTCCCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1805

Oy 585 CACTGCTCCAGTGCAGAAACCAATCAACAGTTGATGCCCAATAACAGCAAGTTCTG 644  
 Db 1806 CACTGCTCCAGTGCAGAAACCAATCAACAGTTGATGCCCAATAACAGCAAGTTCTG 1865  
 Oy 645 AAGCCCACTGCTCTTCTGCTGAGAGGTCCCAAGAGCAATCTGGGCTTT 691  
 Db 1866 AAGCCCACTGCTCTTCTGCTGAGAGGTCCCAAGAGCAATCTGGGCTTT 1912

## RESULT 10

```

US-09-995-898A-22
Sequence 22, Application US/0995898A
Publication No. US20030027253A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Xu, Wenteng
APPLICANT: NO. US20030027253A1ak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FaestSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1422
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zcytor17-Fc4 fusion protein
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1422)
US-09-995-898A-22

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Query Match	Similarity	38.0%	Score	607.4	ID	11	Length	1422
Base	Local	Similarity	99.7%	Pred.	No.	9.5e-168		
Matches	619	Conservative	0	Mismatches	1	Indels	1	Gaps
Qy	67	AGGCCCCGCTCTGCGCCCTCTCCCAAGATGTGACGCTGCTCTCCCAAGACTTCAAGCGGTAC	126					
Db	109	AGGCCCCGCTCTGCGCCCTCTCCCAAGATGTGACGCTGCTCTCCCAAGACTTCAAGCGGTAC	168					
Qy	127	CTGACATGGCTCCCAAGGCTTGGACACCCCAAGATGTGACTTATTTTGGACC-AATCA	185					
Db	169	CTGACATGGCTCCCAAGGCTTGGACACCCCAAGATGTGACTTATTTTGGACTTATTCAG	228					
Qy	186	AGCTCTCCACCGGTACGCGTGGGCGCGAATGTGAAGATGTGCGGAAACCAAGACTG	245					
Db	229	AGCTCTCCACCGGTACGCGTGGGCGCGAATGTGAAGATGTGCGGAAACCAAGACTG	288					
Qy	246	CTATGTTCTAATGATGTGCTGAAAGAAACAGGACTTGTACAAAGTTCAAGGACCGCTG	305					
Db	289	CTATGTTCTAATGATGTGCTGAAAGAAACAGGACTTGTACAAAGTTCAAGGACCGCTG	348					
Qy	306	CGGACGGTTTCTCCCAAGCTCAAGTCCCTCGGTGGTAGTCCGAATTAAGTTAACTT	365					
Db	349	CGGACGGTTTCTCCCAAGCTCAAGTCCCTCGGTGGTAGTCCGAATTAAGTTAACTT	408					
Qy	366	TTTGAAGTGGAGCGGCGCCCACTGCTCTGCTGCTCAACCAAGCGAGGAGATCTCAGT	425					
Db	409	TTTGAAGTGGAGCGGCGCCCACTGCTCTGCTGCTCAACCAAGCGAGGAGATCTCAGT	468					
Qy	426	GGCAATGCCAGTACCAAGCGTGGCCCGCTGACATATGCCCACTGGATCTGAAGTAAAGAGCTG	485					
Db	469	GGCAATGCCAGTACCAAGCGTGGCCCGCTGACATATGCCCACTGGATCTGAAGTAAAGAGCTG	528					
Qy	486	GCAATTCGAGAGAGGGGGGCGGAGAACCAAGACCTATTTCAATCACTCCCATGGCCAG	545					

Accession	Sequence	Position
Db	529 GCATTTCTGGAAAGAGGGGGCCGGAAACAAGACCTTATTTCCAGTCACTTCCCATGGCCAG	5888
Qy	546 CCAGTCCAGATGACTCTTCAGGCCAGCTGGCCAGGAAACACCACTGGCTCAGTGGCCGAACC	6050
Db	589 CCAAGTCCAGATCACTCTTCAGGCCAGCTGGCCAGGAAACCACTGGCTCAGTGGCCGAACC	6488
Qy	606 ATCTACAAGTTCAAGTGTCCGGAATATACGCAAGTTCTTAAGCCCACTGTCTTTGCTG	6658
Db	649 ATCTACAAGTTCAAGTGTCCGGAATATACGCAAGTTCTTAAAGCCCACTGTCTTTGCTG	7080
Qy	666 GAGGTCCAGAGCAAGCAACTGG	686
Db	709 GAGGTCCAGAGCAAGCAACTGG 729	

## RESULT 11

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US-09-995-898A-20
? Sequence 20, Application US/09995898A
? Publication No. US2003027253A1
? GENERAL INFORMATION:
? APPLICANT: Pressnell, Scott R.
? APPLICANT: Xu, Wenfang
? APPLICANT: No. US930027253A1ak, Julia E.
? APPLICANT: Whitmore, Theodore E.
? APPLICANT: Grant, Francis J.
? TITLE OF INVENTION: CYTOKINE RECEPTOR CYT
? FILE REFERENCE: 00-108
? CURRENT APPLICATION NUMBER: US/09/995, 898A
? CURRENT FILING DATE: 2001-11-28
? PRIOR APPLICATION NUMBER: US 60/253,561
? PRIOR FILING DATE: 2000-11-28
? PRIOR APPLICATION NUMBER: US 60/267,211
? PRIOR FILING DATE: 2001-02-07
? NUMBER OF SEQ ID NOS: 50
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 20
? LENGTH: 674
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1) ... (633)
? US-09-995-898A-20

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Query Match#	Local Similarity	31.1%;	Score 498;	DB 11;	Length 674;
Best Local Similarity	99.84;	Score No. 9.1e-136;			
Matches	509;	Conservative	0;	Mismatches	0;
				Indels	1;
				Gaps	1
QY	7	ATGGGGGGGGCCGAGCGCTGGGGGCCCCCTGCTCTGTGCGCTCTGCAAGCCGCTCCAGGG	66		
Db	1	ATGGGGGGGGCCGAGGGCGCTGGGGGCCCCCTGCTCTGTGCTCTGCTCAAGCGGCTCCAGGG	60		
QY	67	AGGCCCCGCTGTGGCGCCCTCCCGAGATGTGACGCTGCTCTCCGAGAACTTCAGCGGTGAC	126		
Db	61	AGGCCCCGCTGTGGCGCCCTCCCGAGATGTGACGCTGCTCTCCCGAGAACTTCAGCGGTGAC	120		
QY	127	CTGACATGCGCTCCGAGGGGTTGGGACGCCCGGACGAGATGTGACTATTGTTGGGCC-ATCAG	185		
Db	121	CTGACATGCGCTCCGAGGGGTTGGGACGCCCGGACGAGATGTGACTATTGTTGGGCTATCAG	180		
QY	186	AGCTCTCCACCCGCTGACGCGTGGCGGAGAGTGTGCGGGAACTCAGAGACTG	245		
Db	181	AGCTCTCCACCCGCTGACGCGTGGCGGAGAGTGTGCGGGAACTCAGAGACTG	240		
QY	246	CTATGTTCTATGATGTGCGCTGAGAGAAACAGAGACTGTAGACAAATTCACAGGACGCGTG	305		
Db	241	CTATGTTCTATGATGTGCGCTGAGAGAAACAGAGACTGTAGACAAATTCACAGGACGCGTG	300		
QY	306	CGGAGCGTTTCTCCGACGCTCCAGTCCCGCCCTGGGTGGAGTCCGAATTAAGTCCGATTAACCTT	365		
Db	301	CGGAGCGTTTCTCCGACGCTCCAGTCCCGCCCTGGGTGGAGTCCGAATTAAGTCCGATTAACCTT	360		

Page 11

Query Match	31.1%	Score 498	DB 14	Length 674
Best Local Similarity	99.8%	Pred. 9.1e-136		
Matches 509	Conservative 0	Mismatches 0	Indels 1	Gaps 1
QY	7	ATGGCGGGGCCCGAGCGCTGGGGCCCCCTGCTCTCTGCTGCTGCTGCTGACGCGCGCTCCAGGG	66	
Db	1	ATGGCGGGGGCCCGAGCGCTGGGGCCCCCTGCTCTCTGCTGCTGCTGCTGACGCGCTCCAGGG	60	
QY	67	AGGCGCCGCTGCGCCCTCCCGAGATGTAGCTGCTCTCCGAGAACTTCAGCGGTGC	126	
Db	61	AGGCGCCGCTGCGCCCTCCCGAGATGTAGCTGCTCTCCGAGAACTTCAGCGGTGC	120	
QY	127	CTGACATGGCTCCGAGAGCTTGGCAACCCCGAGATGTACTTATTTTGGCC-ATGCG	185	
Db	121	CTGACATGGCTCCCGAGAGCTTGGCAACCCCGAGATGTACTTATTTTGGCGCTTACG	180	
QY	186	AGCTCTCCGACCCGTTAGCGGTGGGCGAAGTGTGCGGGACCAAGAGCTG	245	
Db	181	AGCTCTCCGACCCGTTAGCGGTGGGCGAAGTGTGCGGGACCAAGAGCTG	240	
QY	246	CTATGTTCTATGATGTGCTGAGAAACAGGACCTGTATCAACAATTCAAGGACGGTG	305	
Db	241	CTATGTTCTATGATGTGCTGAGAAACAGGACCTGTATCAACAATTCAAGGACGGTG	300	

Query Match	31.1%	Score 498	DB 10	Length 704
Best Local Similarity	99.8%	Pred. No. 9.3e-136		
Matches	509	Conservative 0	Mismatches 0	Indels 1
QY	7	ATGCGGGGGCGGAGCGTGGGGGCCCTGCTCTGTGTCTGTGACGAGCGCTCCAGGG	66	
Db	1	ATGCGGGGGCGGAGCGTGGGGGCCCTGCTCTGTGTCTGTGACGAGCGCTCCAGGG	60	
QY	67	AGGCGCCGCTGTGAGCCCTCTCCGAGATGTGACGCTGCTCCGAGAACTTCAGGTGTAC	126	
Db	61	AGGCGCCGCTGTGAGCCCTCTCCGAGATGTGACGCTGCTCTCCGAGAACTTCAGGTGTAC	120	
QY	127	CTGACATGTGCTCCGAGGGCTTGGCAACCCCGACAGATGTGACCTTATTTTGTGTGCC-ATCAG	185	
Db	121	CTGACATGTGCTCCGAGGGCTTGGCAACCCCGACAGATGTGACCTTATTTTGTGTGTATCAG	180	
QY	186	AGCTCTCCACCCCGTAGACGATGCGCGGAGATGTGAGAGATGTGCGGGAACCAAGAGACTG	245	
Db	181	AGCTCTCCACCCCGTAGACGATGCGCGGAGATGTGAGAGATGTGCGGGAACCAAGAGACTG	240	
QY	246	CTATGTTCTGATGATGTGCTGAGAGAAACAGACCTGTTCACAAAGTTCAGAGGACGCGTG	305	
Db	241	CTATGTTCTGATGATGTGCTGAGAGAAACAGACCTGTTCACAAAGTTCAGAGAGCGCGTG	300	
QY	306	CGAGCGGTTTCTCCGAGCTCAAGTCCCCCTGTGGGTGAGTCCGAACTACGTGATTAACCTT	365	

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Db 301 CGGACGGTCTTCCAGCTCCAGTCCCTGGGTGATGCTCGAATACCTGATTAACCTT 360
Qy 366 TTGAAGTGAAGCCGCGCCACCTGCTCTGATGCTCAACGAGAGAGATCTGAGT 425
Db 361 TTGAAGTGAAGCCGCGCCACCTGCTCTGATGCTCAACGAGAGAGATCTGAGT 420
Qy 426 GCCAATGCCAGTACAGAGTGGCCCCCTGCAATGCCCCCACTGAGATCTGAATGAGAGT 485
Db 421 GCCAATGCCAGTACAGAGTGGCCCCCTGCAATGCCCCCACTGAGATCTGAATGAGAGT 480
Qy 486 GCATTCTGGAAGAGGGGGCCGGAACAG 515
Db 481 GCATTCTGGAAGAGGGGGCCGGAACAG 510
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RESULT 14
US-09-995-898A-29
/ Sequence 29, Application US/09995898A
/ Publication No. US2003027253A1
/ GENERAL INFORMATION:
/ APPLICANT: Preenell, Scott R.
/ APPLICANT: Xu, Wenfeng
/ APPLICANT: No. US2003027253A1ak, Julia B.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Grant, Francis J.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
/ FILE REFERENCE: 00-108
/ CURRENT APPLICATION NUMBER: US/09/995, 898A
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: US 60/253,561
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/267,211
/ PRIOR FILING DATE: 2001-02-07
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 29
/ LENGTH: 633
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Degenerate polynucleotide sequence of SEQ ID NO:21
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(633)
/ OTHER INFORMATION: n = A,T,C or G
US-09-995-898A-29
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Query Match 22.0%; Score 351.2; DB 11; Length 633;
Best Local Similarity 55.6%; Pred. No. 9.7e-93;
Matches 299; Conservative 117; Mismatches 121; Indels 1; Gaps 1;

Qy 7 ATGCGGGGGCCGAGGCGTGGGGCCCTGCTCTGCTGCTGAGAGCGCGTCCAGG 66
Db 1 ATGCGGAGCCGAGGCGTGGGGCCCTGCTCTGCTGCTGAGAGCGCGTCCAGG 60
Qy 67 AGGCGCGGCTGGCGCCCTCCGAGATGAGCGTGTCTCCGAGACTTCCAGCGTGTAC 126
Db 61 MGNCCGNGNTYNGCNCNCNCAAPAYGTNACNTYNTNMSNCAAPAYTTYSNNGTAY 120
Qy 127 CTGACATGAGGCTCCAGGCGTGGCAACCCGAGATGAGCTAATTTGTGGCC-ATGAG 185
Db 121 YTNACNTGTYTNCNGNTYNGNAAATCCNCAAGATGTAACNTAATYTTGTGNCNTAYCAR 180
Qy 186 AGCTCTCCACCCGTAGAGGCTGGCGGCAAGTGAAGATGTGCGGAAACAGAGAGCTG 245
Db 181 MSNNSNCNACNMGNGNNGNTGNGNGARGTNGARAGTGYCNGNGNACNARARATYN 240
Qy 246 CTATGCTTATGATGCTCTGAAGAAAGAGAGCTGTACAAAGTTCAAGAGAGCGCTG 305
Db 241 YTNNGYSNATGATGATGTYTNAAPARCARAGATYTNAAVAATTTAAAGAGNGNTN 300
Cv 306 CGGACGGTCTTCCAGCTCCAGTCCCTGGGTGATGCTCGAATACCTGATTAACCTT 365
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Db 301 MGNACNGTNSNCCNMSNMSNARMSNCCNTGGTNGARNARATYTNATYTN 360
Qy 366 TTGAAGTGAAGCCGCGCCACCTGCTCTGATGCTCAACGAGAGAGATCTGAGT 425
Db 361 TTGAAGTGAAGCCGCGCCACCTGCTCTGATGCTCAACGAGAGAGATCTGAGT 420
Qy 426 GCCAATGCCAGTACAGAGTGGCCCCCTGCAATGCCCCCACTGAGATCTGAATGAGAGT 485
Db 421 GCCAATGCCAGTACAGAGTGGCCCCCTGCAATGCCCCCACTGAGATCTGAATGAGAGT 480
Qy 486 GCATTCTGGAAGAGGGGGCCGGAACAGCCTAATTTCCAGTCACTCCCGAGGCC 543
Db 481 GCATTCTGGAAGAGGGGGCCGGAACAGCCTAATTTCCAGTCACTCCCGAGGCC 538
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RESULT 15
US-10-106-698-3664/C
/ Sequence 3664, Application US/10106698
/ Publication No. US20030109690A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
/ FILE REFERENCE: PA005B1
/ CURRENT APPLICATION NUMBER: US/10/106, 698
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: PatentIn Ver. 3.0
/ SEQ ID NO 3664
/ LENGTH: 634
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (135)..(135)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (211)..(211)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (304)..(304)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (353)..(353)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (534)..(534)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (539)..(539)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (578)..(578)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (581)..(581)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (592)..(592)
/ OTHER INFORMATION: n equals a,c,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (618)..(618)
/ OTHER INFORMATION: n equals a,c,g, or c
US-10-106-698-3664
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Query Match 8.0%; Score 128; DB 14; Length 634;
Best Local Similarity 73.9%; Pred. No. 2.6e-27;
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	Matches	161;	Conservative	0;	Mismatches	57;	Indels	0;	Gaps	0;
Oy	1312	TCC	TGAAAGCTCCCAAGATAA	CTCTCTCTG	GGCCACCTGGGGC	ACTTAC	CAC	1371		
Db	509	TCT	TGAAAGCTCCCAAGATAA	CTCTCTAT	TGGGCCACCTGGGGC	ACTTAC	CAC	450		
Oy	1372	CGA	AGCGAACTGTGTCCCTGGGG	AGCCCAAGTTCTCTT	CAGACACTGAC	CTTCTG	CT	1431		
Db	449	CGA	AGCGAACTGTGTCCCTGGGG	AGCCCAAGTTCTCTT	CAGACACTGAC	CTTCTG	CT	390		
Oy	1432	GGG	AAAGCAGCCCTGAGAGAG	AGAGAGAGGGAATCA	GAATTGAG	ACAGCG	ATG	1491		
Db	389	GGG	AAAGCAGCCCTGAGAGAG	AGAGAGAGGGAATCA	GAATTGAG	ACAGCG	ATG	330		
Oy	1492	CGG	CAGCTGGGGGCTGAGAG	CACCCAGAGACCG	AG			1529		
Db	329	ATT	GAGCCAGAGAGAGAG	ACCAACAACTAC	AG			292		

Search completed: September 18, 2003, 00:22:32  
 Job time : 289.728 secs